```
 M   G   T   P   A   Q   I   L   G   F
ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC
 L   L   L   L   F   P   G   T   R   C
TTG TTG CTC TTG TTT CCA GGT ACC AGA TGT
(leader, -20-1)

 D   I   Q   M   T   Q   S   P   S   S
GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC
 L   S   A   S   L   G   Q   R   V   S
TTA TCT GCC TCT CTG GGA CAA AGA GTC AGT
 L   T   C
CTC ACT TGT  (fr. 1, 1-23)

 R   A   S   Q   D   I   G   I   N   L
CGG GCA AGT CAG GAC ATT GGT ATT AAC TTA
 H
CAT  (cdr1, 24-34)

 T   L   Q   Q   E   P   D   G   T   I
TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT
 K   R   L   I   Y
AAA CGC CTG ATC TAC  (fr2., 35-49)

 A   T   S   S   L   G   S
GCC ACA TCC AGT TTA GGT TCT  (cdr2, 50-56)

 G   V   P   K   R   F   S   G   S   R
GGT GTC CCC AAA AGG TTC AGT GGC AGT AGG
 S   G   S   D   Y   S   L   T   I   S
TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC
 S   L   E   S   G   D   F   V   A   Y
AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT
 Y   C
TAC TGT  (fr3, 57-88)

 L   Q   Y   A   S   S   P   Y   T
CTA CAA TAT GCT AGT TCT CCG TAC ACG
(cdr3, 89-97)
 F   G   G   G   T   K   L   E   I   K
TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA
(fr4, 98-107)

 R   A   D   A   A   P   T   V   S   I
CGG GCT GAT GCT GCA CCA ACT GTA TCC ATC
 F   P   P   S   S   K   L   G
TTC CCA CCA TCC AGT AAG CTT GGG
```

FIG. 1

```
 M   E   C   S   W   V   F   L   F   L   L   S   I   T   T   G   V
ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT GTC
Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly Val

 H   S
CAC TCC
His Ser    (leader)

 Q   A   Y   L   Q   Q   S   G   A   E   L   V   R   S
CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG TCT
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser

 G   A   S   V   K   M   S   C   K   A   S   G   Y   T   L   T
GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG ACC
Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr
(1-30, Fr. #1)

 S   Y   N   M   H
AGT TAC AAT ATG CAC
Ser Tyr Asn Met His  (31-35, CDR 1)

 W   V   K   Q   T   P   G   Q   G   L   E   W   I   G
TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG GAA TGG ATT GGA
Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly
(36-49, Fr. #2)

 N   I   F   P   G   N   G   D   T   Y   Y   N   Q   K   F   K   G
AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT CAG AAG TTT AAG GGC
Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn Gln Lys Phe Lys Gly
(50-66, CDR 2)

 K   A   S   L   T   A   D   T   S   S   S   T   A   Y   M   Q
AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC ACA GCC TAC ATG CAG
Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln

 I   S   S   L   T   S   E   D   S   A   V   Y   F   C   A   R
ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC TAT TTC TGT GCA AGA
Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
(67-98, Fr. #3)

 G   N   W   E   G   A   L   D   Y
GGG AAC TGG GAG GGT GCT CTG GAC TAC
Gly Asn Trp Glu Gly Ala Leu Asp Tyr
(99-107, CDR 3)

 W   G   Q   G   T   S   V   T   V   S   S
TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
(108-118, Fr. #4)

 A   K   T   T   P   P   P   V   Y   P   L   V   P   G   S   L
GCC AAA ACG ACA CCC CCA CCC GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
Ala Lys Thr Thr Pro Pro Pro Val Tyr Pro Leu Val Pro Gly Ser Leu
(constant region)
```

FIG. 2

DIQMTQSPSSLSASLGQRVSLTC — Framework #1, 1–23

RASQDIGINLH — CDR-1, 24–34

TLQQEPDGTIKRLIY — Framework #2, 35–49

ATSSLGS — CDR-2, 50–56

GVPKRFSGSRSGSDYSLTISSLESGDFVAYYC — Framework #3, 57–88

LQYASSPYT — CDR-3, 89–97

FGGGTKLEIK — Framework #4, 98–107

FIG. 3A

QAYLQQSGAELVRSGASVKMSCKASGYTLT — Framework #1, 1–30

SYNMH — CDR-1, 31–35

WVKQTPGQGLEWIG — Framework #2, 36–49

NIFPGNGDTYYNQKFKG — CDR-2, 50–66

KASLTADTSSSTAYMQISSLTSEDSAVYFCAR — Framework #3, 67–98

GNWEGALDY — CDR-3, 99–107

WGQGTSVTVSS — Framework #4, 108–118

FIG. 3B

>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.

```
  67 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
 127 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 186
 187 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTGCCCAAA 246
 247 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
 307 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 366
 367 GGGACCAAGCTGGAAATAAAA 387
```

>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody light chain mRNA.

```
   1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
  61 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
 121 GATGGAACTTTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 180
 181 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTGTCCGTACACGTTCGGAGGG 300
 301 GGGACCAAGCTGGAAATAAAA 321
```

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.

```
 313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
 373 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 432
 433 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 492
 493 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 552
 553 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCGGTGGA 612
 613 GGCACCAAGCTGGAAATCAAA 633
```

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).

```
 314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373
 374 CTCACTTGTCGGCCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 433
 434 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 493
 494 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553
 554 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCGGTGGA 613
 614 GGCACCAAGCTGGAAATCAAA 634
```

>gb|I03643|I03643 Sequence 4 from patent US 4642334.

```
   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
  61 CTCACTTGTCGGCCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
 121 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 180
 181 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCGGTGGA 300
 301 GGCACCAAGCTGGAAATCAAA 321
```

>gb|M59920|MUSIGKAA3 Mouse IG germline chain mRNA V-J region, partial cds.

```
   1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
  61 ACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGAC 120
 121 GGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGG 180
 181 TTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 240
 241 GATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCGGTGGAGGC 300
 301 ACCAAGCTGGAAATCAAA 318
```

FIG. 4A

>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma H220-23.

```
   1 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGT 60
  61 CAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACTATTAAACGC 120
 121 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGG 180
 181 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGACTAT 240
 241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGGGGGACCAAGCTGNAAATA 300
 301 AAA 303
```

>emb|Z22118|MDIGKVBS M.domesticus IgK variable region.

```
   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
  61 CTCACTTGTCGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120
 121 GATGGAACTATTAAACGCCTGATCTACAGCACATCCACTTTAAATTCTGGTGTCCCAAAA 180
 181 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 300
 301 GGGACCAAACTGGAAATAAAA 321
```

>gb|M64168|MUSIGKAFT Mouse Ig active kappa-chain mRNA V-region.

```
   4 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGT 63
  64 CAGGACATTGGTAATAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACTATTAAACGC 123
 124 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGG 183
 184 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAATCTGAAGATTTTGTAGTCTAT 243
 244 TACTGTCTACAATATGCTAGTTATACGTACACGTTCGGAGGGGGGACCAAGTTGGAACTA 303
 304 AAA 306
```

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain(partial) Cloop 1

```
  42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 101
 102 CTCACTTGTCGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
 162 GATGGAACTATTAAACGCCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAA 221
 222 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
 282 GAAGATTTTGCAGACTATTACTGTCTACAATATCTTAGTTATCCGCTCACGTTCGGTGCT 341
 342 GGGACCAAGCTGGAGCTGAAA 362
```

FIG. 4B

```
>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA
                antibody heavy chain mRNA.

   1 CAGGCTTATNTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
  61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
 181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
 241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
 295 ---------------- 311
 312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA
                antibody heavy chain mRNA.

   1 CAGGCTTATGTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
  61 TCCTGCAAGGCTTCTGGCTACAGATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 121 CGTAGACAGGGCCTGGAATGGATTGGAGCAATTTATCCAGGAAATGGTGATACTTCCTAT 180
 181 AATCAGAAGTTCAAGGGCAAGGCCACACTGATTGTAGACAAATCCTCCAGCACAGCCTAC 240
 241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGAGA 298
 299 GGGGTAACTACGTAGGACATATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357
 358 TCA 360

>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain,
                variable region.

   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTAAGGCCTGGGTCCTCAGTGAAGATG 60
  61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
 181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
 241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGGAT 300
 301 TACTCCGGTAGTATAGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 354

>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.

  96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
 156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
 216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
 276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
 336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
 393 ---------------------------------- 427
 428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

>gb|I05921|I05921 Sequence 37 from patent EP 0274394.

  96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
 156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
 216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
 276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
 336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
 393 ------------------------------- 427
 428 CTGGGGCACAGGGACCACGGTCACCGTCTC 457
```

FIG. 5A

```
>emb|Z22117|MDIGGVBC M.domesticus IgG variable region.
     2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATAT 61
    62 CCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTGAAGCAGAAGC 121
   122 CTGGGCAGGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTAATACTTACTACA 181
   182 ATGAGAAGTTCAAGGGYAAGGCCTCACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 241
   242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGACGTTACT 301
   302 ------------ 314
   315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma
                    VDJ4 region of J558 family mRNA.
     1 CAGGTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
    61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
   121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
   181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
   241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAG 295
   296 ------------------ 314
   315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJ4
                    region of J558 family mRNA.
     1 CAGGTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
    61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
   121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
   181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
   241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
   295 ---------------------- 317
   318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

>gb|M15225|MUSIGLAG H-chain lambda rearranged anti-Dns hybridoma VDJ4 region
                    of J558 family mRNA.
     1 CAGGTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
    61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
   121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
   181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240
   241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
   295 ---------------- 311
   312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

>gb|M20835|MUSIGKCLP Mouse IgMk rearranged heavy-chain mRNA variable region
                    (V-D-J) anti-DNA autoantibody.
   106 CAGGTCCAACTGCAGCAGCCTGGTGCTGAGCTTGTGAAGCCTGGGGCCTCAGTGAAGCTG 165
   166 TCCTGCAAGGCTTCTGGCTACACTTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGG 225
   226 CCTGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTAGTAGTACTAACTAC 285
   286 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 345
   346 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACG 401
   402 -------------- 416
   417 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 462
```


FIG. 5B

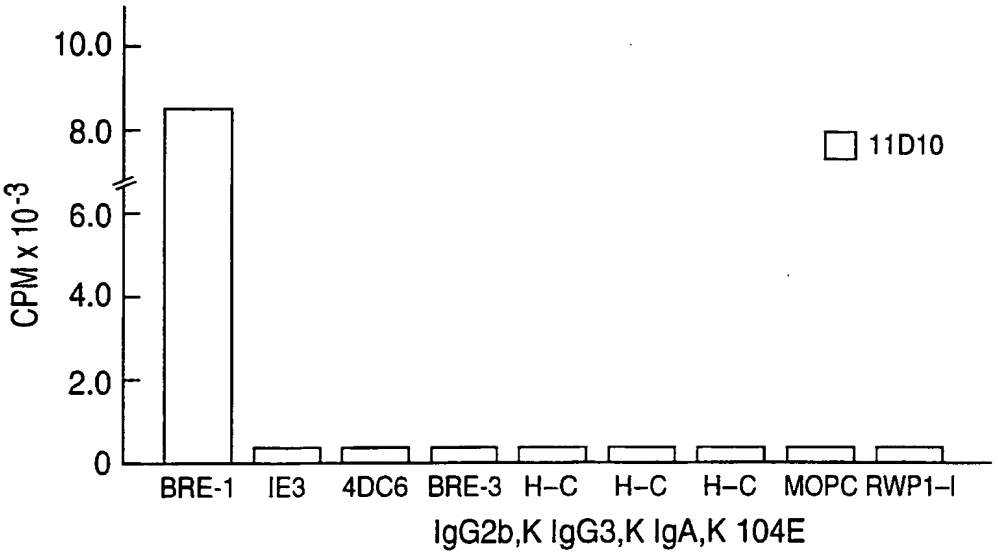

FIG. 6

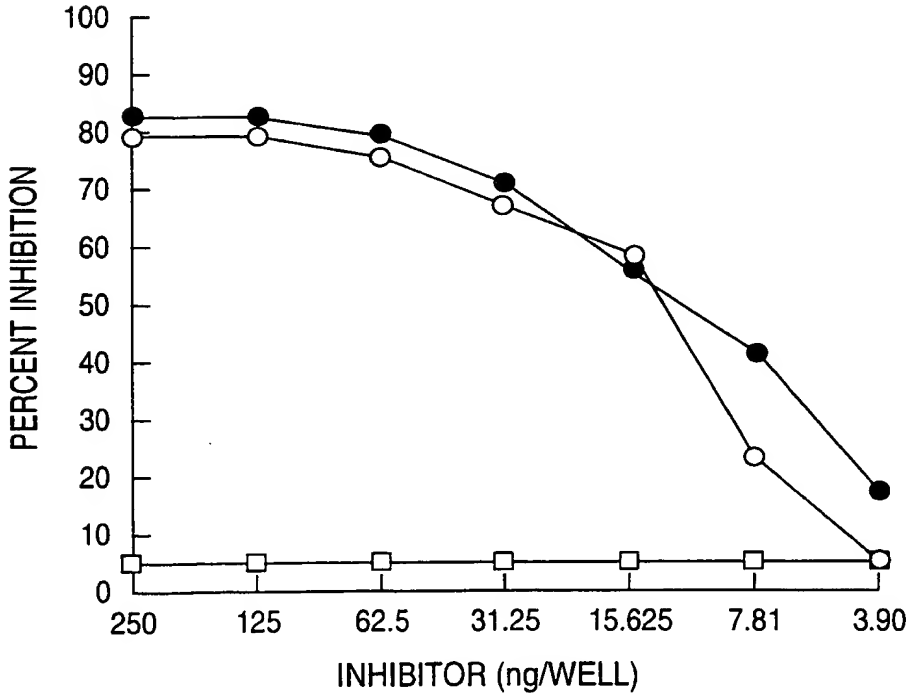

FIG. 7

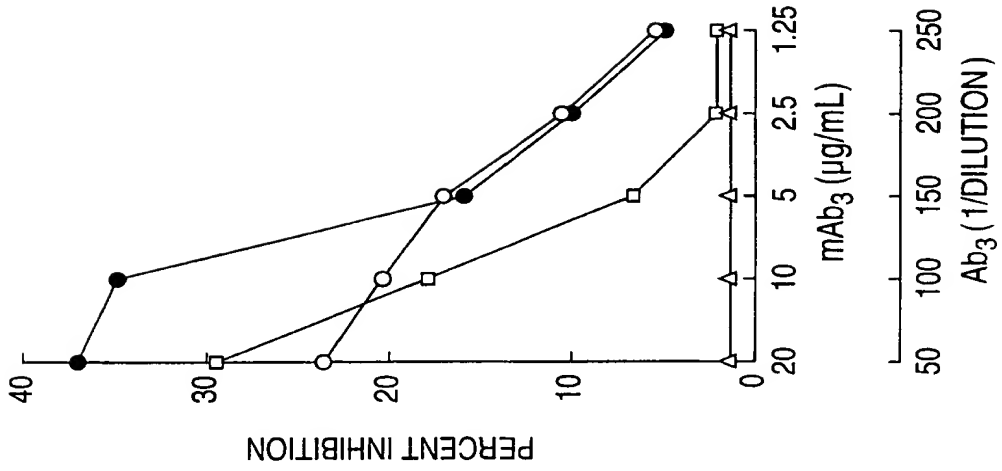

FIG. 9

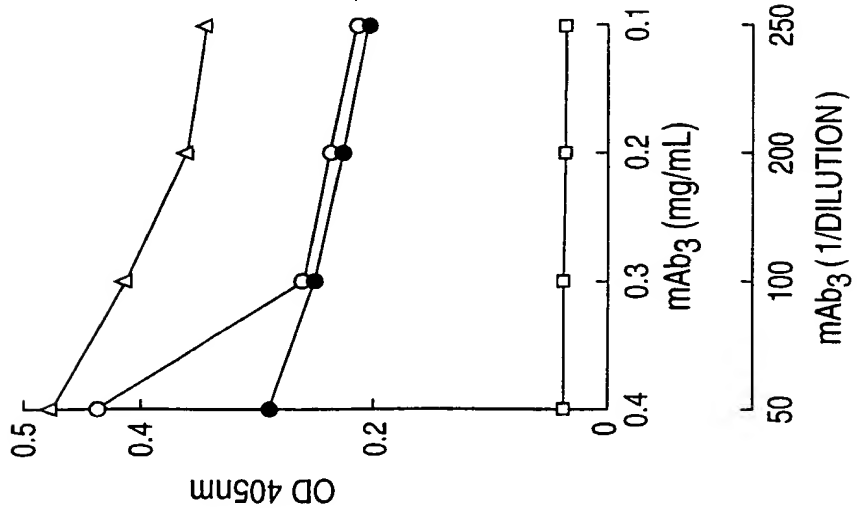

FIG. 8

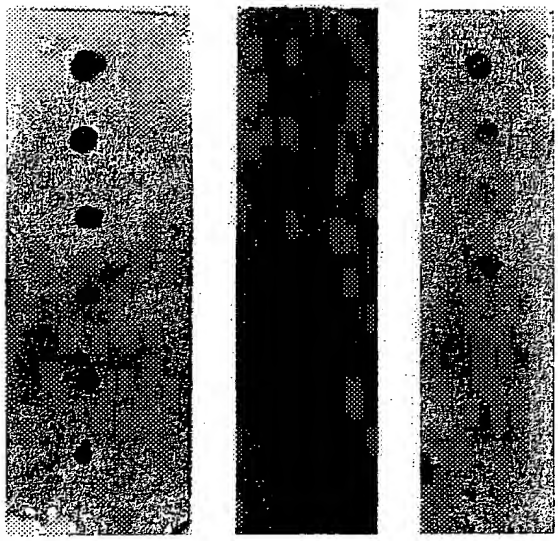

FIG. 10

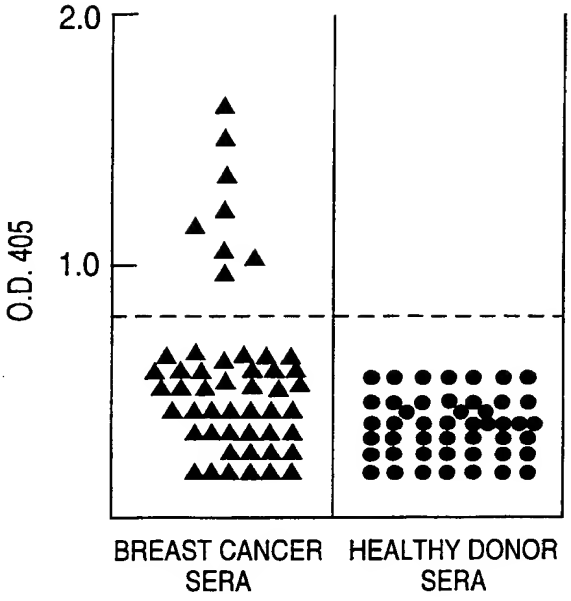

FIG. 11

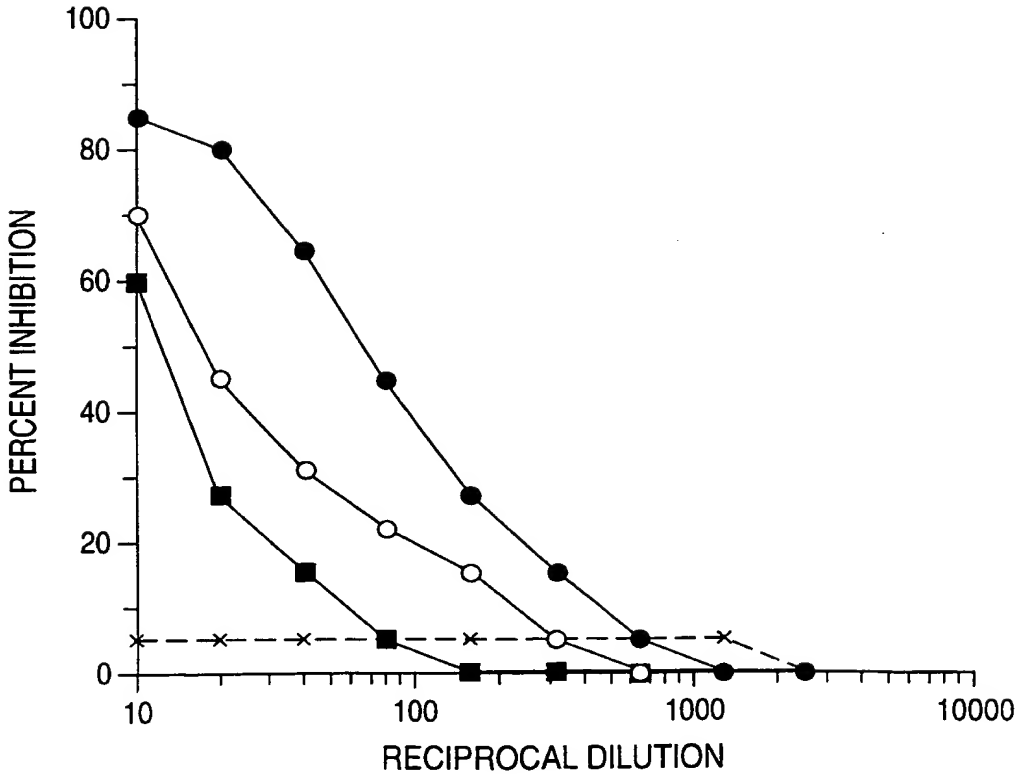

FIG. 12

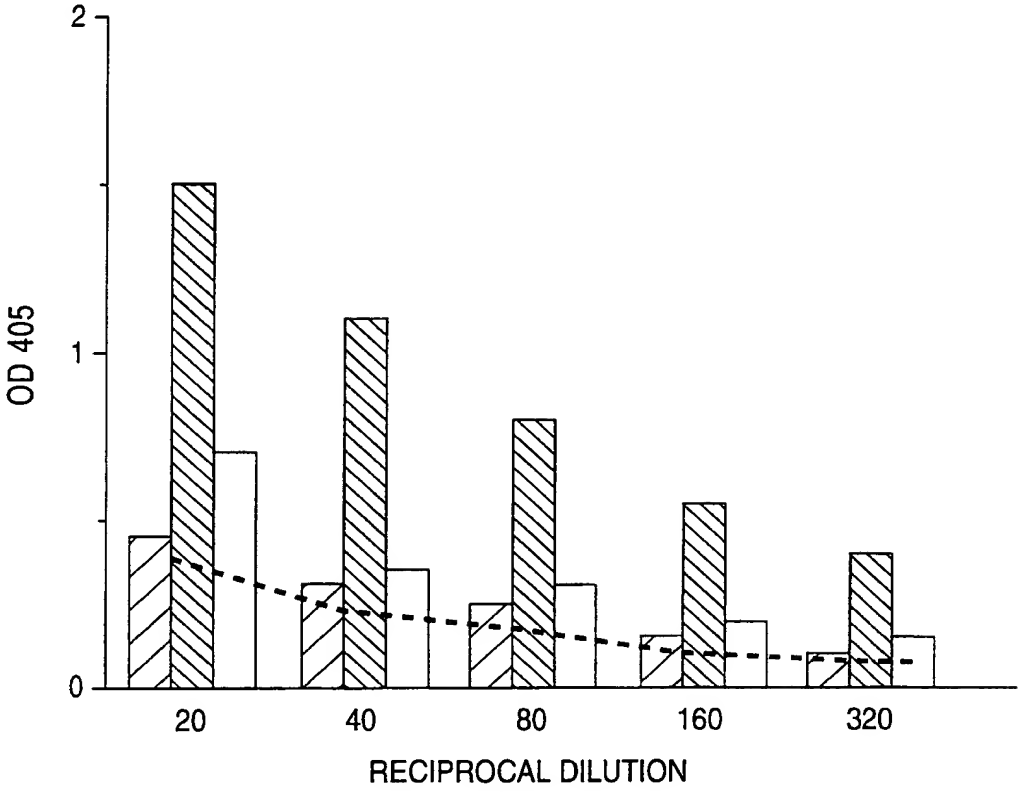

FIG. 13

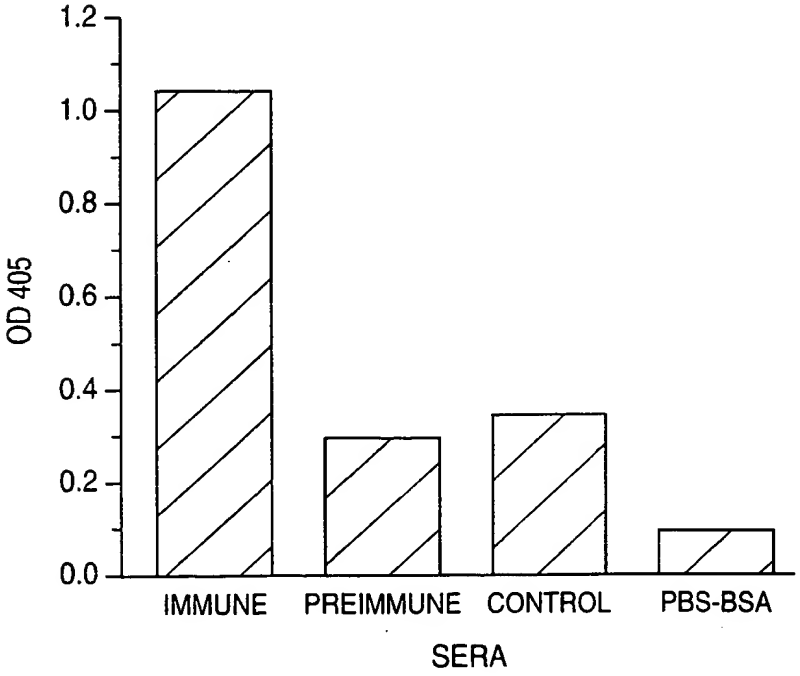

FIG. 14

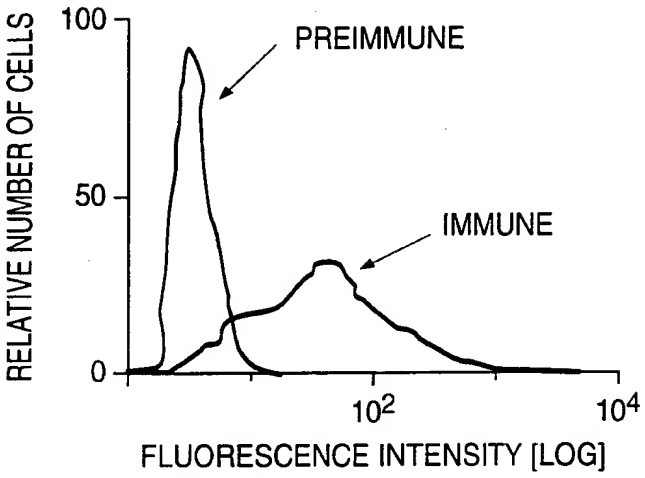

FIG. 15A

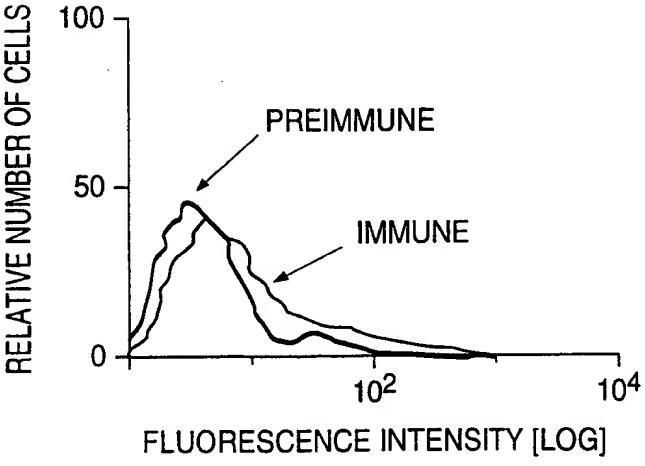

FIG. 15B

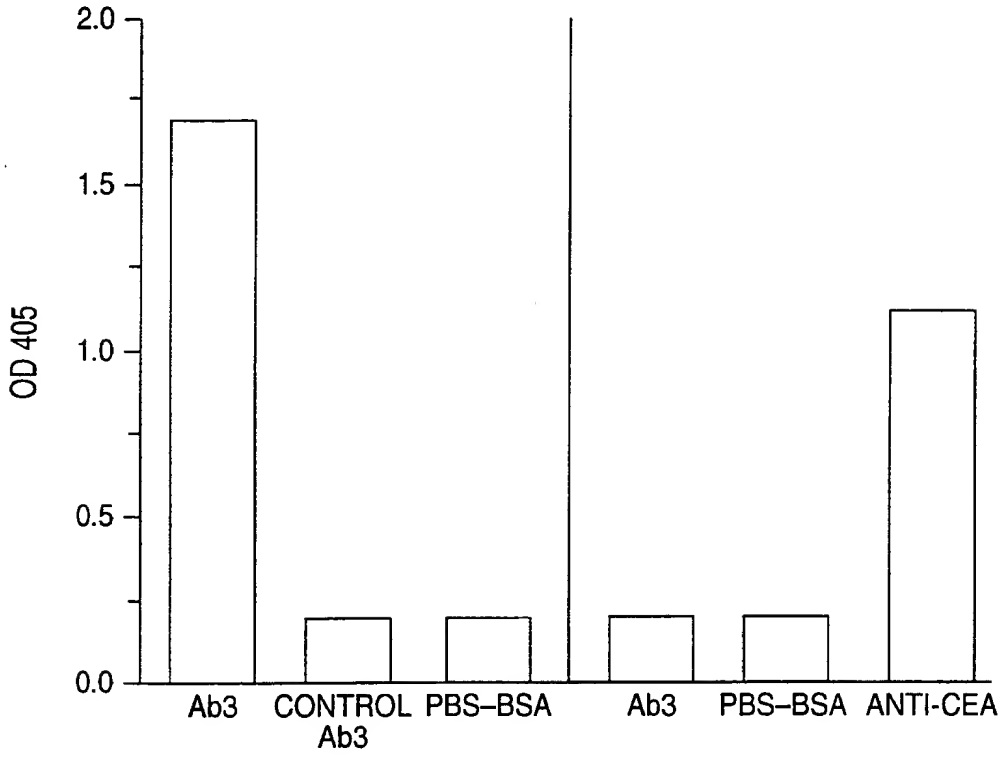

FIG. 16

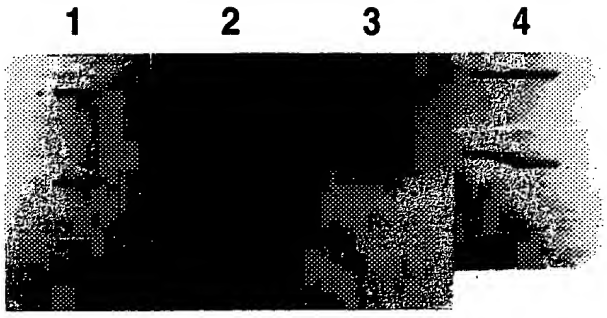

FIG. 17

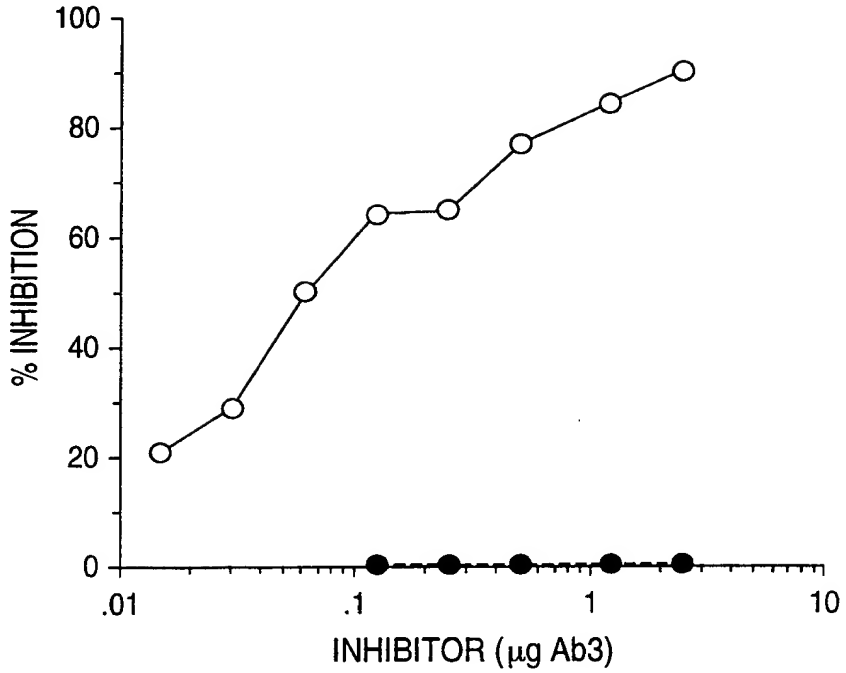

FIG. 18

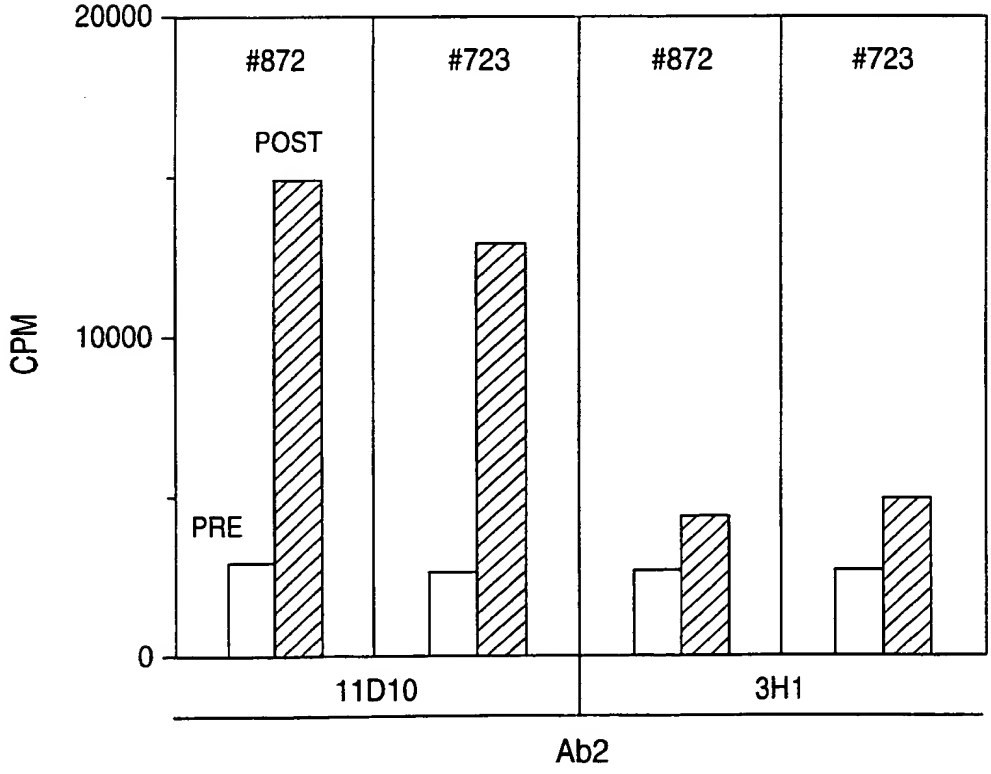

FIG. 19

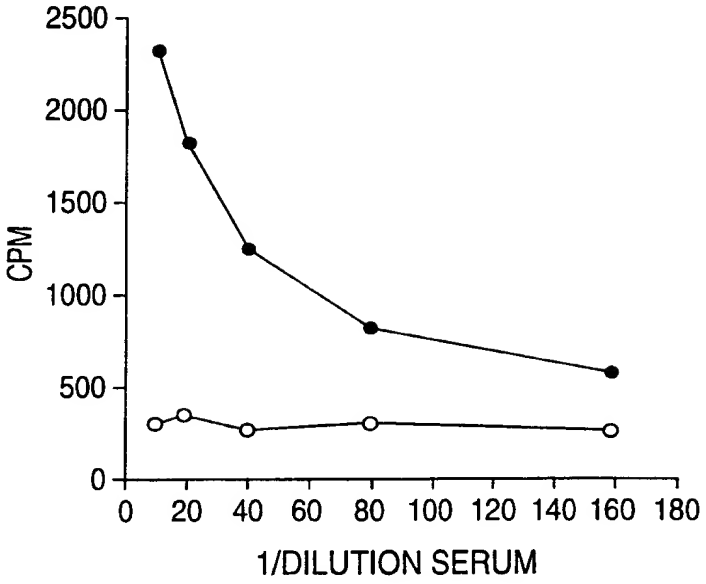

FIG. 20

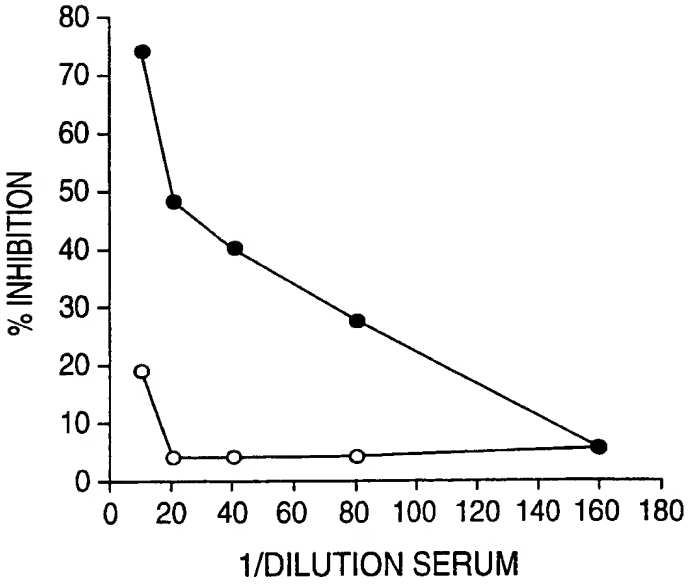

FIG. 21

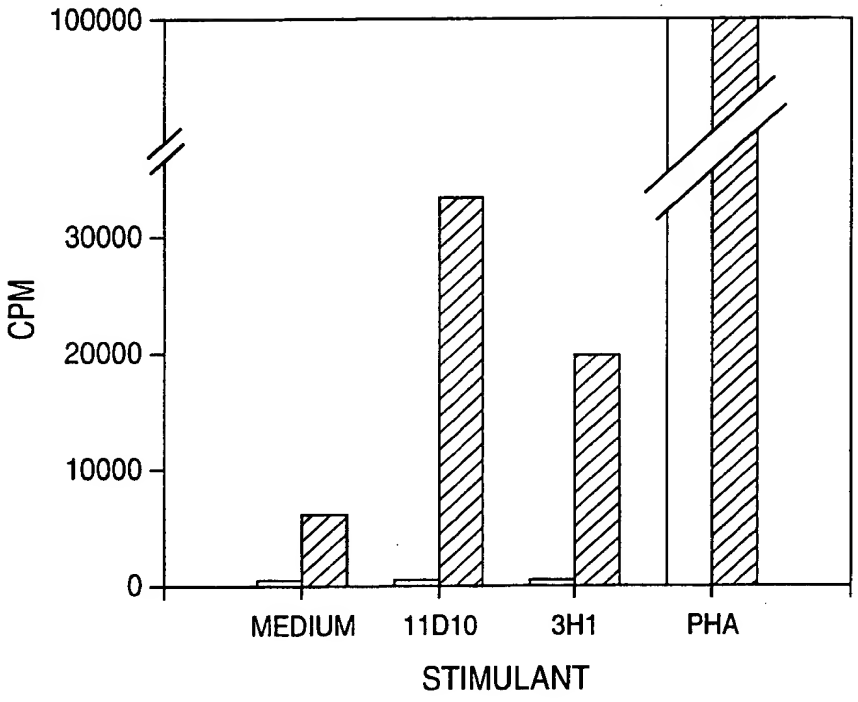

FIG. 22

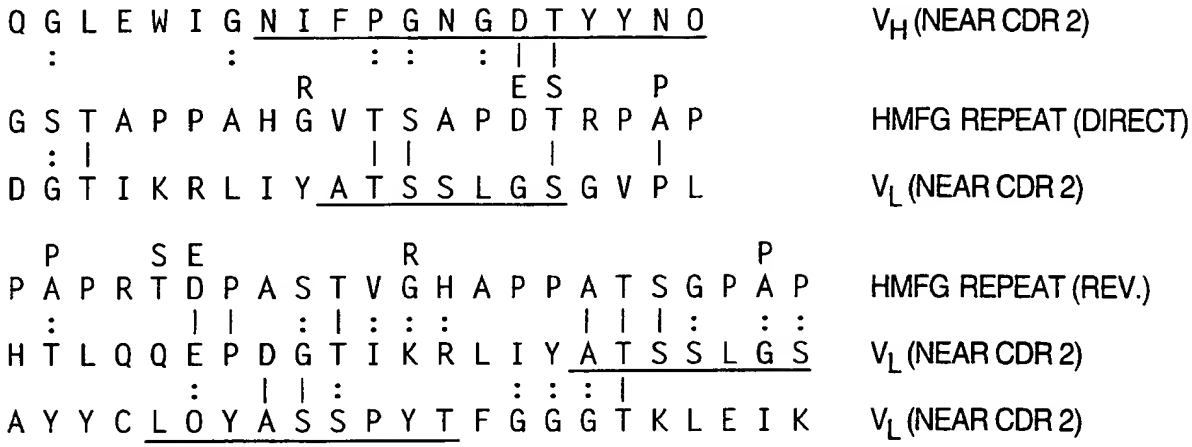

FIG. 23

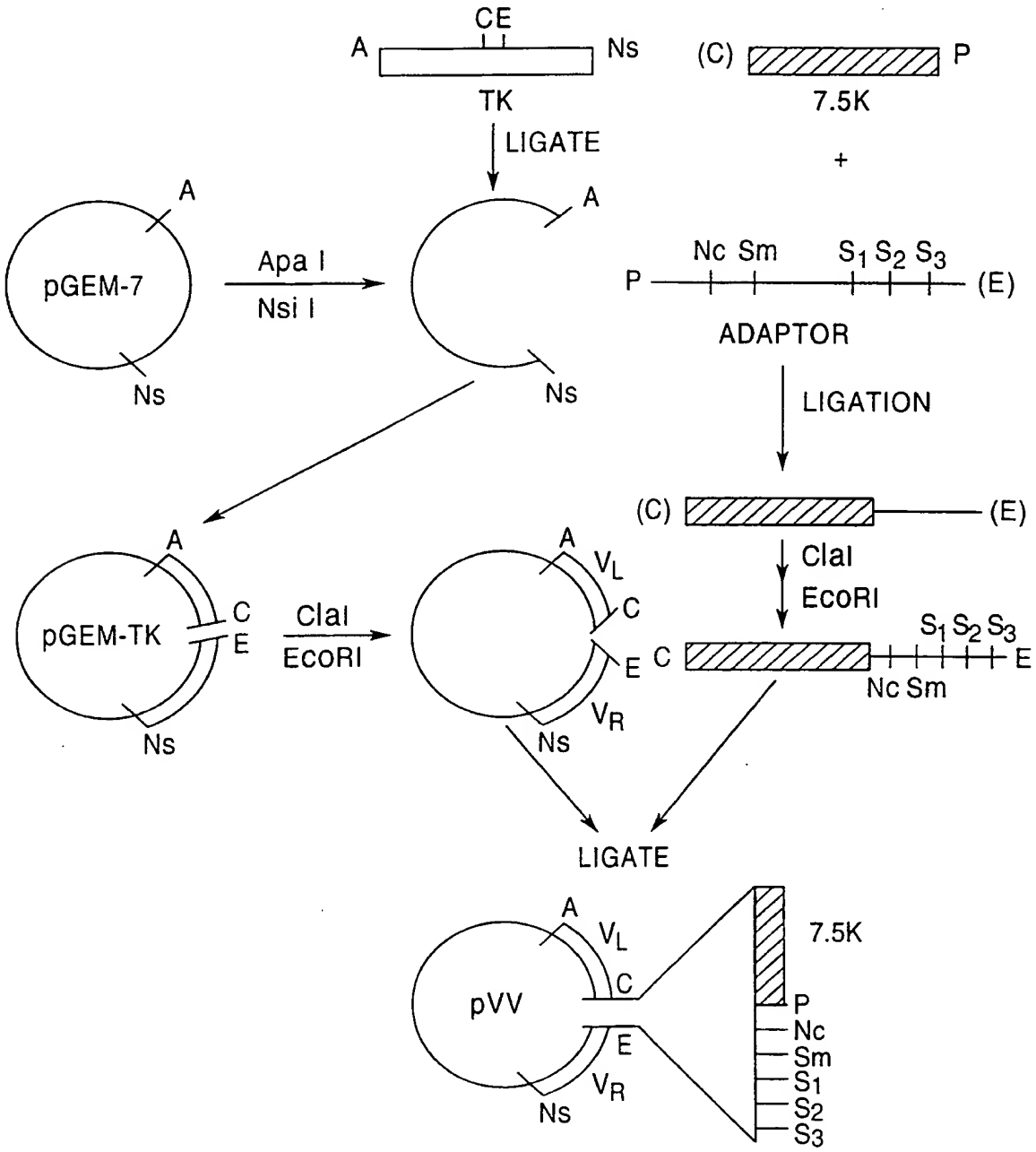

FIG. 24

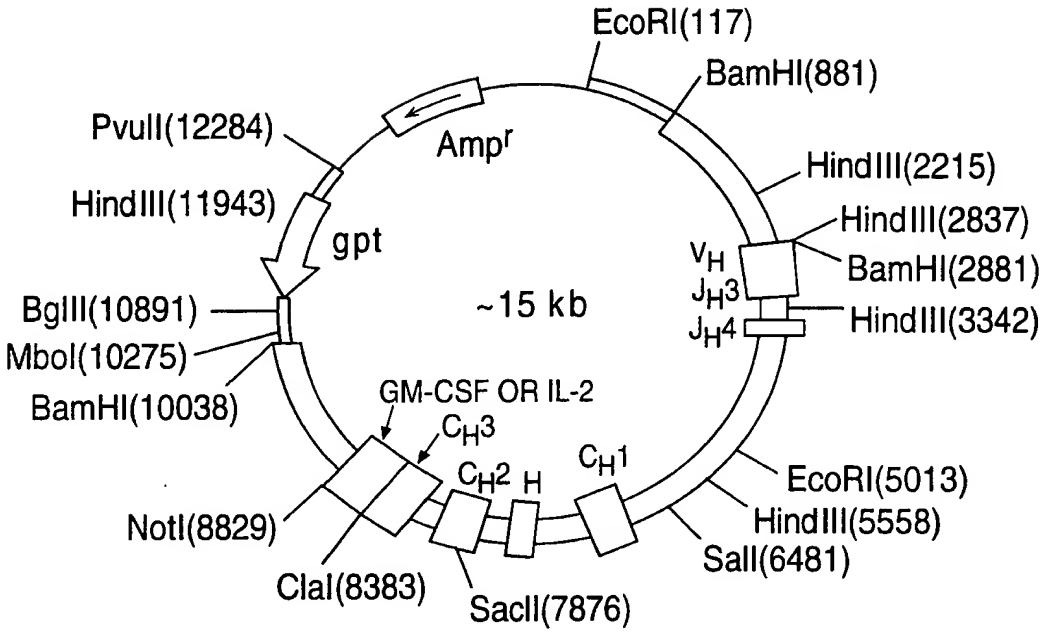

FIG. 25A

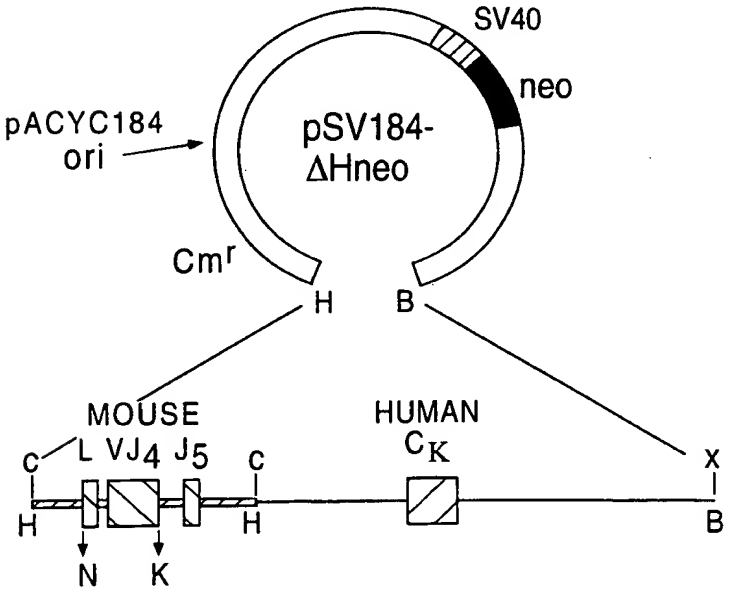

FIG. 25B

```
11D10: 1   DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

 1     23  ..............E.............SS.NW.................D..... 82
 2     23  ..............E.............SS.NW.................D..... 82
 3     23  ..............E.............SS.NW.................D..... 82
 4     23  ..............E.......P.....SS.NW.................D..... 82
 5      1  ..............E.............SS.NW.................D..... 60
 6      1  ..............E.............SS.NW.................D..... 59
 7      1  ..............E.............RS.NW.................D..... 60
 8      1  ..............E.........E.SGY.SW...K.........S..T.N..... 60
 9      1  ..........E.............SS.NW.................D..... 54
10      1  ..............E.........E.SGY.SW...K...........A.T.D..... 60
11      1  X.........E.............NS.NW.................D..... 55
12      1  ..............E....A.....E..GY.SW...K...........A.T.D..... 60
13     14  ..............E.........E.SGY.SW...K...........A.T.D..... 73
14      1  EL............E.........E.SGY.SW...K...........A.T.D..... 60
15      2  ELVL..........E.........E.NGY.GW...K...........A.T.H..... 61


11D10: 61  RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIK  107

 1     83  ........................D.....................  129
 2     83  ........................D.........W...........  129
 3     83  ........................D.........W...........  129
 4     83  ........................D.........W...........  129
 5     61  ........................D.........W...........  106
 6     60  ........................D.........W...........  106
 7     61  ........................D.......T..W...........  106
 8     61  ........................AD.....................  107
 9     55  ........................D...................X..  107
10     60  ........................AD.....................  106
11     56  ........................V........YT..........L.  102
12     61  ..G.....................AD........Y.W...........  106
13     74  ........................AD......L.Y.L...A.....L.  120
14     61  ........................AD........Y.L...A.....L.  107
15     62  ........................AD........Y.R...........  108
```

FIG. 26A

```
11D10:  1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY  60

 1      1 ..:.........P.S.........F.........R.....A.Y.....S.  60
 2     20 ............P............F.........R.....A.Y.....S.  79
 3      1 EVQ.....P...KP.....I.....F.D.Y.....K.....E.Y..S.N...  60
 4      1 .IQ.....P....P.....I.....F.D.YI.....R..E.....W.Y..S.N.K.  60
 5      1 .VQ.....P...KP.....L.....F.D.TI.....S.....W.Y..S.N.K.  60
 6      1 .VQ..E.....KP.....L.....F...W.....R.....K.N.S..R.N.  60
 7     20 .VQ.....AKP............F.A.W.....R.....Y.N.NT.Y.E.  79
 8      1 EVQ.....KP.....L.....F...W.....R.....E.D.SDSY...  60
 9      1 .VQ....E...A.P..........F.R.W.....R...A.....A.Y...S..N.  60
10      1 .VQ.....P.T...I.....F.N.WLG....R..H.....D.Y..G.Y.N.  60
11     20 .VQ.....AKP............F...R.....R.....Y.N.ST.Y.E.  79
12      1 .VQ.....AKP............F...W.....R.....Y.N.ST.Y.E.  60
13      1 .IQ.....P....P.....I.....F.D.YI.....R..E.....W.Y..S.N.K.  60
14      1 .VQ.....P.T.....A...F.N.WIG....R..H.....D.Y..G.Y.N.  60
15      1 EVQ.....TV.A.P..........F...W.....R.....A.Y...S..R.  60


11D10: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG==NWEG===ALDYWGQGTSVTVSS 118

 1     61 .....T..V.K.....L.............==DYS.===SI.....TL....  118
 2     80 .....T..V.K.....L.............xxxxxxxxx=xx.V..T..T....  140
 3     61 .E.....K.....L.............xxxxxxx===.M.....  120
 4     61 .E.....T..V.....L.............===xxx===.M.....  117
 5     61 .D.....TM...K.....L.............=VAR.S==.M.....  119
 6     61 .E...S..T..V.K.....L.....Y....xxxxxxxxx.....T.....  123
 7     80 ..N..D..T....K.....L.....Y.T.xxx.Y..===.M.....  139
 8     61 .....T..V.K.....F.....Y...xxxxxxx===xM.....  120
 9     61 .....K...V..A.....EL...A.....Y...S==RYR.===SM.....  119
10     61 .E.....T.....L.....P==HYY.===SG.....TL....  118
11     80 .....D..T....K.....L....F.....Y....====x.===VF.....TL....  135
12     61 .....D..T....K.....L.....L.Y...W==VYYY===.M.....  118
13     61 .E.....T..V.....L.....===xxx===.M.....  117
14     61 .E.....T.....L.....I.Y...P==FYFY===.M.....C....  118
15     61 .....K...V..A.....EL....N.....Y.T..==GLFT===.M.....  115
```

FIG. 26B

Light Chain

```
                                          ***********                 *******
VL consensus: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDSGVPK 60
11D10:        1 ...............Q.............IN.HT...................G..... 60

HMFG fragments:                                                GSIAPPAHRVTSAPESRPPP
                                                          ppprsepastvrhappatsg


                                                 *********
VL consensus:   61  RFSGSRSGSDYSLTISSLESGDFVDYYCLQYASSPYTFGGGTKLEIK  107
11D10:          61  ......................A.....................  107

HMFG fragments:                                  ppprsepastvrhappatsg
```

Heavy Chain

```
                                              *****               ***********
VH consensus: 1 QVQLQQSGAELVRPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNGDTNY 60
11D10:        1 .AY.........S.............L...N......T.........N.F......Y. 60

HMFG fragments:                                                    APDTRPPP


                   ******                                 *********
VH consensus: 61 NQKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGxxxGAMDYWGQGTSVTVSS 118
11D10:        61 ........S.............I................NWE..L............. 118
```

FIG. 26C

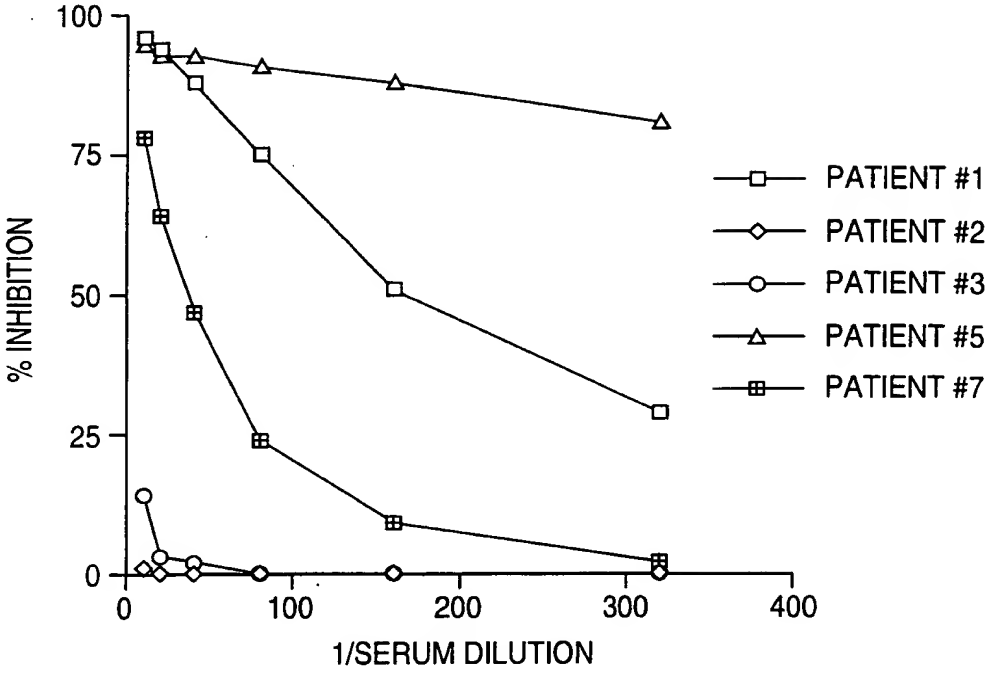

FIG. 27A

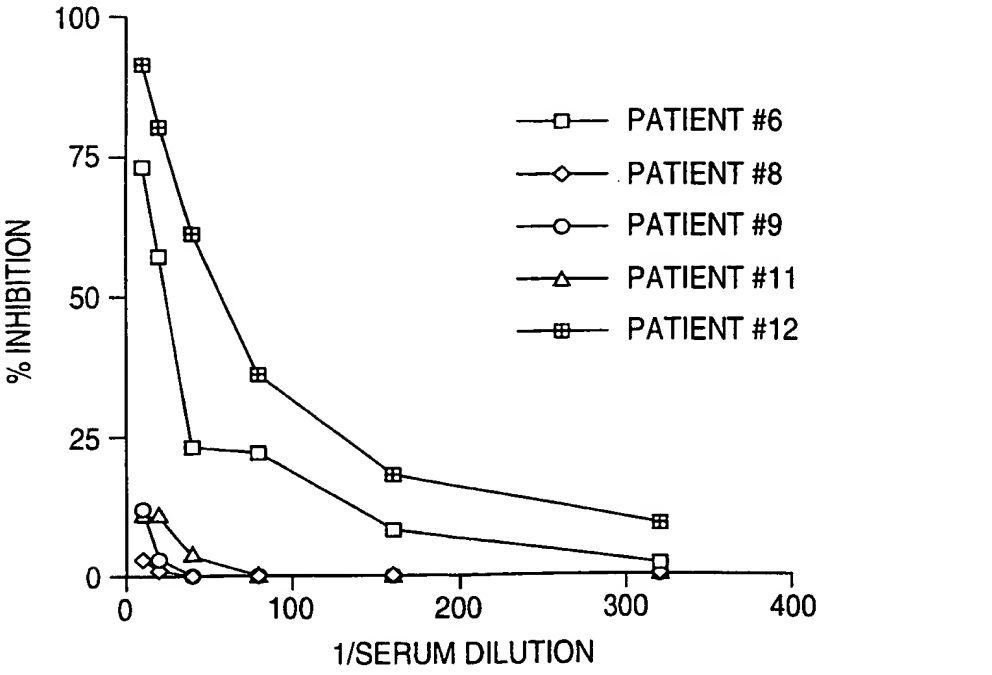

FIG. 27B

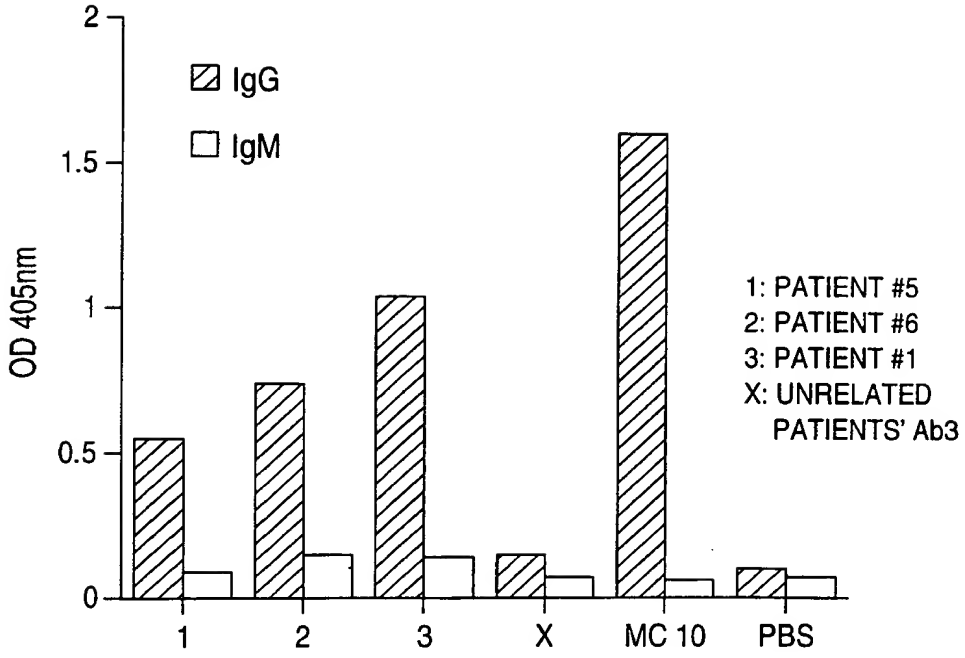

FIG. 28

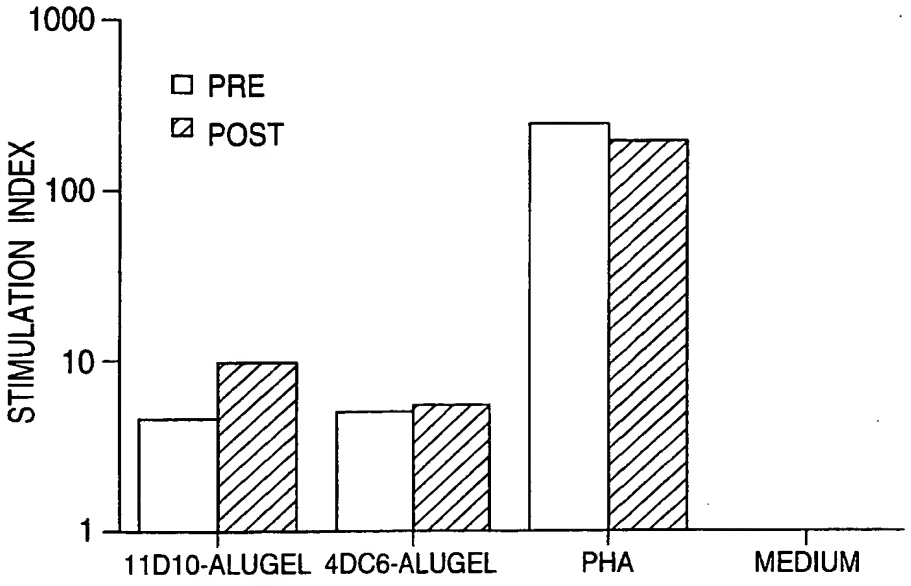

FIG. 29A

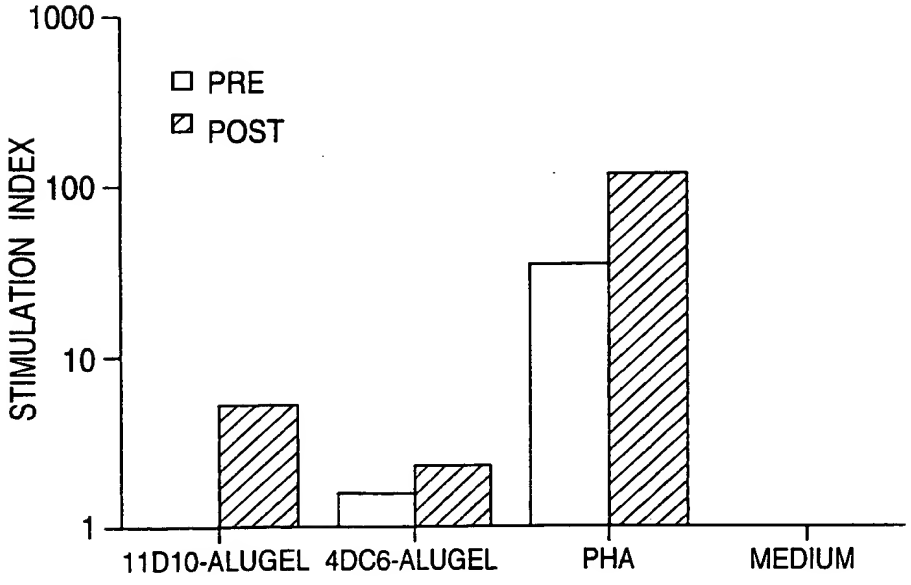

FIG. 29B